

UNITED STATES PATENT AND TRADEMARK OFFICE
CERTIFICATE OF CORRECTION

PATENT NO. : 6,872,546 B1
DATED : March 29, 2005
INVENTOR(S) : Hastings et al.

Page 1 of 60

It is certified that error appears in the above-identified patent and that said Letters Patent is hereby corrected as shown below:

Title page.

Item [56], **References Cited, OTHER PUBLICATIONS**, fourth reference should read:
-- Lee et al., "A novel secretory Tumor Necrosis Factor-inducible Protein (TSG-6) is a member of the family of Hyaluronate Binding Proteins, closely related to the Adhesion Receptor CD44" Jan. 1992, vol. 116, No. 2, pp. 545-557.* --.

Column 315.

Starting at line 36, before claims, insert the attached sequence listing.

Column 317.

Lines 11-19, delete the second subsets (a)-(g).

Column 318.

Line 9, after "claim 33," insert -- wherein said --.

Signed and Sealed this

Fourth Day of April, 2006



JON W. DUDAS
Director of the United States Patent and Trademark Office

SEQUENCE LISTING

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aca atg gtc act tgt acc tgc ctg ccc gac tac gag ggt gat ggc tgg	5314
Thr Met Val Thr Cys Thr Cys Leu Pro Asp Tyr Glu Gly Asp Gly Trp	
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agc tgc cgg gcc cgc aac ccc tgc aca gat ggc cac cgc ggg ggc tgc	5362
Ser Cys Arg Ala Arg Asn Pro Cys Thr Asp Gly His Arg Gly Gly Cys	
1720 1725 1730	
agc gag cac gcc aac tgc ttg agc acc ggc ctg aac aca cgg cgc tgt	5410
Ser Glu His Ala Asn Cys Leu Ser Thr Gly Leu Asn Thr Arg Arg Cys	
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gag tgc cac gca ggc tac gta ggc gat gga ctg cag tgt ctg gag gag	5458
Glu Cys His Ala Gly Tyr Val Gly Asp Gly Leu Gln Cys Leu Glu Glu	
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tcg gaa cca cct gtg gac cgc tgc ttg ggc cag cca ccg ccc tgc cac	5506
Ser Glu Pro Pro Val Asp Arg Cys Leu Gly Gln Pro Pro Pro Cys His	
1765 1770 1775	
tca gat gcc atg tgc act gac ctg cac ttc cag gag aaa cgg gct ggc	5554
Ser Asp Ala Met Cys Thr Asp Leu His Phe Gln Glu Lys Arg Ala Gly	
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gtt ttc cac ctc cag gcc acc agc ggc cct tat ggt ctg aac ttt tcg	5602
Val Phe His Leu Gln Ala Thr Ser Gly Pro Tyr Gly Leu Asn Phe Ser	
1800 1805 1810	
gag gct gag gcg gca tgc gaa gca cag gga gcc gtc ctt gct tca ttc	5650
Glu Ala Glu Ala Ala Cys Glu Ala Gln Gly Ala Val Leu Ala Ser Phe	
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cct cag ctc tct gct gcc cag cag ctg ggc ttc cac ctg tgc ctc atg	5698
Pro Gln Leu Ser Ala Ala Gln Gln Leu Gly Phe His Leu Cys Leu Met	
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ggc tgg ctg gcc aat ggc tcc act gcc cac cct gtg gtt ttc cct gtg	5746
Gly Trp Leu Ala Asn Gly Ser Thr Ala His Pro Val Val Phe Pro Val	
1845 1850 1855	

gcf gac tgt ggc aat ggt cgg gtg ggc ata gtc agc ctg ggt gcc cgc Ala Asp Cys Gly Asn Gly Arg Val Gly Ile Val Ser Leu Gly Ala Arg 1860 1865 1870 1875	5794
aag aac ctc tca gaa cgc tgg gat gcc tac tgc ttc cgt gtg caa gat Lys Asn Leu Ser Glu Arg Trp Asp Ala Tyr Cys Phe Arg Val Gln Asp 1880 1885 1890	5842
gtg gcc tgc cga tgc cga aat ggc ttc gtg ggt gac ggg atc agc acg Val Ala Cys Arg Cys Arg Asn Gly Phe Val Gly Asp Gly Ile Ser Thr 1895 1900 1905	5890
tgc aat ggg aag ctg ctg gat gtg ctg gct gcc act gcc aac ttc tcc Cys Asn Gly Lys Leu Leu Asp Val Leu Ala Ala Thr Ala Asn Phe Ser 1910 1915 1920	5938
acc ttc tat ggg atg cta ttg ggc tat gcc aat gcc acc cag cgg ggt Thr Phe Tyr Gly Met Leu Leu Gly Tyr Ala Asn Ala Thr Gln Arg Gly 1925 1930 1935	5986
ctc gac ttc ctg gac ttc ctg gat gat gag ctc acg tat aag aca ctc Leu Asp Phe Leu Asp Phe Leu Asp Asp Glu Leu Thr Tyr Lys Thr Leu 1940 1945 1950 1955	6034
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cca aac ttg gag ctg cat gcc tcc aac gcc acc ctc cta agt gcc aac Pro Asn Leu Glu Leu His Ala Ser Asn Ala Thr Leu Leu Ser Ala Asn 1975 1980 1985	6130
gcc agc cag ggg aag ttg ctt ccg gcc cac tca ggc ctc agc ctc atc Ala Ser Gln Gly Lys Leu Leu Pro Ala His Ser Gly Leu Ser Leu Ile 1990 1995 2000	6178
atc agt gac gca ggc cct gac aac agt tcc tgg gcc cct gtg gcc cca Ile Ser Asp Ala Gly Pro Asp Asn Ser Ser Trp Ala Pro Val Ala Pro 2005 2010 2015	6226

ggg aca gtt gtg gtt agc cgt atc att gtg tgg gac atc atg gcc ttc	6274
Gly Thr Val Val Val Ser Arg Ile Ile Val Trp Asp Ile Met Ala Phe	
2020 2025 2030 2035	
aat ggc atc atc cat gct ctg gcc agc ccc ctc ctg gca ccc cca cag	6322
Asn Gly Ile Ile His Ala Leu Ala Ser Pro Leu Leu Ala Pro Pro Gln	
2040 2045 2050	
ccc cag gca gtg ctg gcg ctt gaa gcc cca cct gtg gcg gca ggc gtg	6370
Pro Gln Ala Val Leu Ala Xaa Glu Ala Pro Pro Val Ala Ala Gly Val	
2055 2060 2065	
ggg gct gtg ctt gcc gct gga gca ctg ctt ggc ttg gtg gcc gga gct	6418
Gly Ala Val Leu Ala Ala Gly Ala Leu Leu Gly Leu Val Ala Gly Ala	
2070 2075 2080	
ctc tac ctc cgt gcc cga ggc aag ccc atg ggc ttt ggc ttc tct gcc	6466
Leu Tyr Leu Arg Ala Arg Gly Lys Pro Met Gly Phe Gly Phe Ser Ala	
2085 2090 2095	
ttc cag gcg gaa gat gat gct gat gac gan ttc tca ccg tgg caa gaa	6514
Phe Gln Ala Glu Asp Asp Ala Asp Asp Xaa Phe Ser Pro Trp Gln Glu	
2100 2105 2110 2115	
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Gly Thr Asn Pro Xaa Leu Xaa Xaa Val Pro Asn Pro Val Phe Gly Ser	
2120 2125 2130	
gac acc ttt tgt gaa ccc ttc gat gac tca ctg ctg gag gag gac ttc	6610
Asp Thr Phe Cys Glu Pro Phe Asp Asp Ser Leu Leu Glu Glu Asp Phe	
2135 2140 2145	
cct gac acc cag agg atc ctc aca gtc aag tga cgaggctggg gctgaaagca	6663
Pro Asp Thr Gln Arg Ile Leu Thr Val Lys	
2150 2155	
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Ala Ser Leu Ala Gln Gln Leu Cys Arg Gln His Ile Ile Ala Gly Gln
35 40 45

His Ile Leu Glu Asp Thr Arg Thr Gln Gln Thr Arg Arg Trp Trp Thr
50 55 60

Leu Ala Gly Gln Glu Ile Thr Val Thr Phe Asn Gln Phe Thr Lys Tyr
65 70 75 80

Ser Tyr Lys Tyr Lys Asp Gln Pro Gln Gln Thr Phe Asn Ile Tyr Lys
85 90 95

Ala Asn Asn Ile Ala Ala Asn Gly Val Phe His Val Val Thr Gly Leu
100 105 110

Arg Trp Gln Ala Pro Ser Gly Thr Pro Gly Asp Pro Lys Arg Thr Ile
115 120 125

Gly Gln Ile Leu Ala Ser Thr Glu Ala Phe Ser Arg Phe Glu Thr Ile
130 135 140

Leu Glu Asn Cys Gly Leu Pro Ser Ile Leu Asp Gly Pro Gly Pro Phe
145 150 155 160

Thr Val Phe Ala Pro Ser Asn Glu Ala Val Asp Ser Leu Arg Asp Gly
165 170 175

Arg Leu Ile Tyr Leu Phe Thr Ala Gly Leu Ser Lys Leu Gln Glu Leu
180 185 190

Val Arg Tyr His Ile Tyr Asn His Gly Gln Leu Thr Val Glu Lys Leu
195 200 205

Ile Ser Lys Gly Arg Ile Leu Thr Met Ala Asn Gln Val Leu Ala Val
210 215 220

Asn Ile Ser Glu Glu Gly Arg Ile Leu Leu Gly Pro Glu Gly Val Pro
225 230 235 240

Leu Gln Arg Val Asp Val Met Ala Ala Asn Gly Val Ile His Met Leu
245 250 255

Asp Gly Ile Leu Leu Pro Pro Thr Ile Leu Pro Ile Leu Pro Lys His
260 265 270

Cys Ser Glu Glu Gln His Lys Ile Val Ala Gly Ser Cys Val Asp Cys
275 280 285

Gln Ala Leu Asn Thr Ser Thr Cys Pro Pro Asn Ser Val Lys Leu Asp
290 295 300

Ile Phe Pro Lys Glu Cys Val Tyr Ile His Asp Pro Thr Gly Leu Asn
305 310 315 320

Val Leu Lys Lys Gly Cys Ala Ser Tyr Cys Asn Gln Thr Ile Met Glu
325 330 335

Gln Gly Cys Cys Lys Gly Phe Phe Gly Pro Asp Cys Thr Gln Cys Pro
340 345 350

Gly Gly Phe Ser Asn Pro Cys Tyr Gly Lys Gly Asn Cys Ser Asp Gly
355 360 365

Ile Gln Gly Asn Gly Ala Cys Leu Cys Phe Pro Asp Tyr Lys Gly Ile
370 375 380

Ala Cys His Ile Cys Ser Asn Pro Asn Lys His Gly Glu Gln Cys Gln
385 390 395 400

Glu Asp Cys Gly Cys Val His Gly Leu Cys Asp Asn Arg Pro Gly Ser
405 410 415

Gly Gly Val Cys Gln Gln Gly Thr Cys Ala Pro Gly Phe Ser Gly Arg
420 425 430

Phe Cys Asn Glu Ser Met Gly Asp Cys Gly Pro Thr Gly Leu Ala Gln
435 440 445

His Cys His Leu His Ala Arg Cys Val Ser Gln Glu Gly Val Ala Arg
450 455 460

Cys Arg Cys Leu Asp Gly Phe Glu Gly Asp Gly Phe Ser Cys Thr Pro
465 470 475 480

Ser Asn Pro Cys Ser His Pro Asp Arg Gly Gly Cys Ser Glu Asn Ala
485 490 495

Glu Cys Val Pro Gly Ser Leu Gly Thr His His Cys Thr Cys His Lys
500 505 510

Gly Trp Ser Gly Asp Gly Arg Val Cys Val Ala Ile Asp Glu Cys Glu
515 520 525

Leu Asp Val Arg Gly Gly Cys His Thr Asp Ala Leu Cys Ser Tyr Val
530 535 540

Gly Pro Gly Gln Ser Arg Cys Thr Cys Lys Leu Gly Phe Ala Gly Asp
545 550 555 560

Gly Tyr Gln Cys Ser Pro Ile Asp Pro Cys Arg Ala Gly Asn Gly Gly
565 570 575

Cys His Gly Leu Glu Leu Glu Ala Asn Ala His Phe Ser Ile Phe Tyr
580 585 590

Gln Trp Leu Lys Ser Ala Gly Ile Thr Leu Pro Ala Asp Arg Arg Val
595 600 605

Thr Ala Leu Val Pro Ser Glu Ala Ala Val Arg Gln Leu Ser Pro Glu
610 615 620

Asp Arg Ala Phe Trp Leu Gln Pro Arg Thr Leu Pro Asn Leu Val Arg
625 630 635 640

Ala His Phe Leu Gln Gly Ala Leu Phe Glu Glu Glu Leu Ala Arg Leu
645 650 655

Gly Gly Gln Glu Val Ala Thr Leu Asn Pro Thr Thr Arg Trp Glu Ile
660 665 670

Arg Asn Ile Ser Gly Arg Val Trp Val Gln Asn Ala Ser Val Asp Val
675 680 685

Ala Asp Leu Leu Ala Thr Asn Gly Val Leu His Ile Leu Ser Gln Val
690 695 700

Leu Leu Pro Pro Arg Gly Asp Val Pro Gly Gly Gln Gly Leu Leu Gln
705 710 715 720

Gln Leu Asp Leu Val Pro Ala Phe Ser Leu Phe Arg Glu Leu Leu Gln
725 730 735

His His Gly Leu Val Pro Gln Ile Glu Ala Ala Thr Ala Tyr Thr Ile
740 745 750

Phe Val Pro Thr Asn Arg Ser Leu Glu Ala Gln Gly Asn Ser Ser His
755 760 765

Leu Asp Ala Asp Thr Val Arg His His Val Val Leu Gly Glu Ala Leu
770 775 780

Ser Met Glu Thr Leu Arg Lys Gly Gly His Arg Asn Ser Leu Leu Gly
785 790 795 800

Pro Ala His Trp Ile Val Phe Tyr Asn His Ser Gly Gln Pro Glu Val
805 810 815

Asn His Val Pro Leu Glu Gly Pro Met Leu Glu Ala Pro Gly Arg Ser
820 825 830

Leu Ile Gly Leu Ser Gly Val Leu Thr Val Gly Ser Ser Arg Cys Leu
835 840 845

His Ser His Ala Glu Ala Leu Arg Glu Lys Cys Val Asn Cys Thr Arg
850 855 860

Arg Phe Arg Cys Thr Gln Gly Phe Gln Leu Gln Asp Thr Pro Arg Lys
865 870 875 880

Ser Cys Val Tyr Arg Ser Gly Phe Ser Phe Ser Arg Gly Cys Ser Tyr
885 890 895

Thr Cys Ala Lys Lys Ile Gln Val Pro Asp Cys Cys Pro Gly Phe Phe
900 905 910

Gly Thr Leu Cys Glu Pro Cys Pro Gly Gly Leu Gly Gly Val Cys Ser
915 920 925

Gly His Gly Gln Cys Gln Asp Arg Phe Leu Gly Ser Gly Glu Cys His
930 935 940

Cys His Glu Gly Phe His Gly Thr Ala Cys Glu Val Cys Glu Leu Gly
945 950 955 960

Arg Tyr Gly Pro Asn Cys Thr Gly Val Cys Asp Cys Ala His Gly Leu
965 970 975

Cys Gln Glu Gly Leu Gln Gly Asp Gly Ser Cys Val Cys Asn Val Gly
980 985 990

Trp Gln Gly Leu Arg Cys Asp Gln Lys Ile Thr Ser Pro Gln Cys Pro
995 1000 1005

Arg Lys Cys Asp Pro Asn Ala Asn Cys Val Gln Asp Ser Ala Gly Ala
1010 1015 1020

Ser Thr Cys Ala Cys Ala Ala Gly Tyr Ser Gly Asn Gly Ile Phe Cys
1025 1030 1035 1040

Ser Glu Val Asp Pro Cys Ala His Gly His Gly Gly Cys Ser Pro His
1045 1050 1055

Ala Asn Cys Thr Lys Val Ala Pro Gly Gln Arg Thr Cys Thr Cys Gln
1060 1065 1070

Asp Gly Tyr Met Gly Asp Gly Glu Leu Cys Gln Glu Ile Asn Ser Cys
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Leu Ile His His Gly Gly Cys His Ile His Ala Glu Cys Ile Pro Thr
1090 1095 1100

Gly Pro Gln Gln Val Ser Cys Ser Cys Arg Glu Gly Tyr Ser Gly Asp
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Gly Ile Arg Thr Cys Glu Leu Leu Asp Pro Cys Ser Lys Asn Asn Gly
1125 1130 1135

Gly Cys Ser Pro Tyr Ala Thr Cys Lys Ser Thr Gly Asp Gly Gln Arg
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Phe Thr Ile Phe Val Pro His Ala Asp Leu Met Ser Asn Leu Ser Gln
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Asp Glu Leu Ala Arg Ile Arg Ala His Arg Gln Leu Val Phe Arg Tyr
1220 1225 1230

His Val Val Gly Cys Arg Arg Leu Arg Ser Glu Asp Leu Leu Glu Gln
1235 1240 1245

Gly Tyr Ala Thr Ala Leu Ser Gly His Pro Leu Arg Phe Ser Glu Arg
1250 1255 1260

Glu Gly Ser Ile Tyr Leu Asn Asp Phe Ala Arg Val Val Ser Ser Asp
1265 1270 1275 1280

His Glu Ala Val Asn Gly Ile Leu His Phe Ile Asp Arg Val Leu Leu
1285 1290 1295

Pro Pro Glu Ala Leu His Trp Glu Pro Asp Asp Ala Pro Ile Pro Arg
1300 1305 1310

Arg Asn Val Thr Ala Ala Ala Gln Gly Phe Gly Tyr Lys Ile Phe Ser
1315 1320 1325

Gly Leu Leu Lys Val Ala Gly Leu Leu Pro Leu Leu Arg Glu Ala Ser
1330 1335 1340

His Arg Pro Phe Thr Met Leu Trp Pro Thr Asp Ala Ala Phe Arg Ala
1345 1350 1355 1360

Leu Pro Pro Asp Arg Gln Ala Trp Leu Tyr His Glu Asp His Arg Asp
1365 1370 1375

Lys Leu Ala Ala Ile Leu Arg Gly His Met Ile Arg Asn Val Glu Ala
1380 1385 1390

Leu Ala Ser Asp Leu Pro Asn Leu Gly Pro Leu Arg Thr Met His Gly
1395 1400 1405

Thr Pro Ile Ser Phe Ser Cys Ser Arg Thr Arg Pro Gly Glu Leu Met
1410 1415 1420

Val Gly Glu Asp Asp Ala Arg Ile Val Gln Arg His Leu Pro Phe Glu
1425 1430 1435 1440

Gly Gly Leu Ala Tyr Gly Ile Asp Gln Leu Leu Glu Pro Pro Gly Leu
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Gly Ala Arg Cys Asp His Phe Glu Thr Arg Pro Leu Arg Leu Asn Thr
1460 1465 1470

Cys Ser Ile Cys Gly Leu Glu Pro Pro Cys Pro Glu Gly Ser Gln Glu
1475 1480 1485

Gln Gly Ser Pro Glu Ala Cys Trp Arg Phe Tyr Pro Lys Phe Trp Thr
1490 1495 1500

Ser Pro Pro Leu His Ser Leu Gly Leu Arg Ser Val Trp Val His Pro
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Ser Leu Trp Gly Arg Pro Gln Gly Leu Gly Arg Gly Cys His Arg Asn
1525 1530 1535

Cys Val Thr Thr Thr Trp Lys Pro Ser Cys Cys Pro Gly His Tyr Gly
1540 1545 1550

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1555 1560 1565

Arg Gly Val Cys Met Asp Gly Met Ser Gly Ser Gly Gln Cys Leu Cys
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Phe Gly Pro His Cys Gln Ala Cys Arg Cys Thr Val His Gly Arg Cys
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1620 1625 1630

Thr Gly Pro Arg Cys Glu Val Gln Leu Glu Leu Gln Pro Val Cys Thr
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Pro Pro Cys Ala Pro Glu Ala Val Cys Arg Ala Gly Asn Ser Cys Glu
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Cys Ser Leu Gly Tyr Glu Gly Asp Gly Arg Val Cys Thr Val Ala Asp
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Leu Cys Gln Asp Gly His Gly Gly Cys Ser Glu His Ala Asn Cys Ser
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Gln Val Gly Thr Met Val Thr Cys Thr Cys Leu Pro Asp Tyr Glu Gly
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Gly Gly Cys Ser Glu His Ala Asn Cys Leu Ser Thr Gly Leu Asn Thr
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Arg Arg Cys Glu Cys His Ala Gly Tyr Val Gly Asp Gly Leu Gln Cys
1745 1750 1755 1760

Leu Glu Glu Ser Glu Pro Pro Val Asp Arg Cys Leu Gly Gln Pro Pro
1765 1770 1775

Pro Cys His Ser Asp Ala Met Cys Thr Asp Leu His Phe Gln Glu Lys
1780 1785 1790

Arg Ala Gly Val Phe His Leu Gln Ala Thr Ser Gly Pro Tyr Gly Leu
1795 1800 1805

Asn Phe Ser Glu Ala Glu Ala Ala Cys Glu Ala Gln Gly Ala Val Leu
1810 1815 1820

Ala Ser Phe Pro Gln Leu Ser Ala Ala Gln Gln Leu Gly Phe His Leu
1825 1830 1835 1840

Cys Leu Met Gly Trp Leu Ala Asn Gly Ser Thr Ala His Pro Val Val
1845 1850 1855

Phe Pro Val Ala Asp Cys Gly Asn Gly Arg Val Gly Ile Val Ser Leu
1860 1865 1870

Gly Ala Arg Lys Asn Leu Ser Glu Arg Trp Asp Ala Tyr Cys Phe Arg
1875 1880 1885

Val Gln Asp Val Ala Cys Arg Cys Arg Asn Gly Phe Val Gly Asp Gly
1890 1895 1900

Ile Ser Thr Cys Asn Gly Lys Leu Leu Asp Val Leu Ala Ala Thr Ala
1905 1910 1915 1920

Asn Phe Ser Thr Phe Tyr Gly Met Leu Leu Gly Tyr Ala Asn Ala Thr
1925 1930 1935

Gln Arg Gly Leu Asp Phe Leu Asp Phe Leu Asp Asp Glu Leu Thr Tyr
1940 1945 1950

Lys Thr Leu Phe Val Pro Val Asn Glu Gly Phe Val Asp Asn Met Thr
1955 1960 1965

Leu Ser Gly Pro Asn Leu Glu Leu His Ala Ser Asn Ala Thr Leu Leu
1970 1975 1980

Ser Ala Asn Ala Ser Gln Gly Lys Leu Leu Pro Ala His Ser Gly Leu
1985 1990 1995 2000

Ser Leu Ile Ile Ser Asp Ala Gly Pro Asp Asn Ser Ser Trp Ala Pro
2005 2010 2015

Val Ala Pro Gly Thr Val Val Val Ser Arg Ile Ile Val Trp Asp Ile
2020 2025 2030

Met Ala Phe Asn Gly Ile Ile His Ala Leu Ala Ser Pro Leu Leu Ala
2035 2040 2045

Pro Pro Gln Pro Gln Ala Val Leu Ala Xaa Glu Ala Pro Pro Val Ala
2050 2055 2060

Ala Gly Val Gly Ala Val Leu Ala Ala Gly Ala Leu Leu Gly Leu Val
2065 2070 2075 2080

Ala Gly Ala Leu Tyr Leu Arg Ala Arg Gly Lys Pro Met Gly Phe Gly
2085 2090 2095

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Trp Gln Glu Gly Thr Asn Pro Xaa Leu Xaa Xaa Val Pro Asn Pro Val
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Lys Gly His Val Cys Ala Ala Gly Trp Met Ala Lys Gly Arg Val Gly
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Tyr Val Lys Gly Asn Cys Gly Gly Lys Thr Gly Asp Tyr Gly Arg Asn
65 70 75 80

Arg Ser Arg Trp Asp Ala Tyr Cys Tyr Asn His Ala Lys Cys Gly Gly
85 90 95

Val Thr Asp Lys Arg Lys Ser Gly Asn Tyr Asp Asn Cys Tyr Trp His
100 105 110

Arg Lys Tyr Gly Arg His Ser Asp Asp Asp Asp Gly Cys Ala Asp Tyr
115 120 125

Val Tyr Asp Ser Tyr Asp Asp Val His Gly Val Gly Arg Tyr Cys Gly
130 135 140

Asp Asp Asp Ser Thr Gly Asn Val Met Thr Lys Ser Asp Ala Ser Val
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Asp Tyr Glu Gly Asp Gly Trp Ser Cys Arg Ala Arg Asn Pro Cys Thr	
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gat ggc cac cgc ggg ggc tgc agc gag cac gcc aac tgc ttg agc acc	150
Asp Gly His Arg Gly Gly Ser Glu His Ala Asn Cys Leu Ser Thr	
25 30 35 40	
ggc ctg aac aca cgg cgc tgt gag tgc cac gca ggc tac gta ggc gat	198
Gly Leu Asn Thr Arg Arg Cys Glu Cys His Ala Gly Tyr Val Gly Asp	
45 50 55	
gga ctg cag tgt ctg gag gag tcg gaa cca cct gtg gac cgc tgc ttg	246
Gly Leu Gln Cys Leu Glu Glu Ser Glu Pro Pro Val Asp Arg Cys Leu	
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ggc cag cca ccg ccc tgc cac tca gat gcc atg tgc act gac ctg cac	294
Gly Gln Pro Pro Pro Cys His Ser Asp Ala Met Cys Thr Asp Leu His	
75 80 85	
ttc cag gag aaa cgg gct ggc gtt ttc cac ctc cag gcc acc agc ggc	342
Phe Gln Glu Lys Arg Ala Gly Val Phe His Leu Gln Ala Thr Ser Gly	
90 95 100	
cct tat ggt ctg aac ttt tcg gag gct gag gcg gca tgc gaa gca cag	390
Pro Tyr Gly Leu Asn Phe Ser Glu Ala Ala Cys Glu Ala Gln	
105 110 115 120	
gga gcc gtc ctt gct tca ttc cct cag ctc tct gct gcc cag cag ctg	438
Gly Ala Val Leu Ala Ser Phe Pro Gln Leu Ser Ala Ala Gln Gln Leu	
125 130 135	
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Gly Phe His Leu Cys Leu Met Gly Trp Leu Ala Asn Gly Ser Thr Ala	
140 145 150	
cac cct gtg gtt ttc cct gtg gcg gac tgt ggc aat ggt cgg gtg ggc	534
His Pro Val Val Phe Pro Val Ala Asp Cys Gly Asn Gly Arg Val Gly	
155 160 165	

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Ile Val Ser Leu Gly Ala Arg Lys Asn Leu Ser Glu Arg Trp Asp Ala	
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Tyr Cys Phe Arg Val Gln Asp Val Ala Cys Arg Cys Arg Asn Gly Phe	
185 190 195 200	
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Val Gly Asp Gly Ile Ser Thr Cys Asn Gly Lys Leu Leu Asp Val Leu	
205 210 215	
gct gcc act gcc aac ttc tcc acc ttc tat ggg atg cta ttg ggc tat	726
Ala Ala Thr Ala Asn Phe Ser Thr Phe Tyr Gly Met Leu Leu Gly Tyr	
220 225 230	
gcc aat gcc acc cag cgg ggt ctc gac ttc ctg gac ttc ctg gat gat	774
Ala Asn Ala Thr Gln Arg Gly Leu Asp Phe Leu Asp Phe Leu Asp Asp	
235 240 245	
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Glu Leu Thr Tyr Lys Thr Leu Phe Val Pro Val Asn Glu Gly Phe Val	
250 255 260	
gac aac atg acg ctg agt ggc cca aac ttg gag ctg cat gcc tcc aac	870
Asp Asn Met Thr Leu Ser Gly Pro Asn Leu Glu Leu His Ala Ser Asn	
265 270 275 280	
gcc acc ctc cta agt gcc aac gcc agc cag ggg aag ttg ctt ccg gcc	918
Ala Thr Leu Leu Ser Ala Asn Ala Ser Gln Gly Lys Leu Leu Pro Ala	
285 290 295	
cac tca ggc ctc agc ctc atc atc agt gac gca ggc cct gac aac agt	966
His Ser Gly Leu Ser Leu Ile Ile Ser Asp Ala Gly Pro Asp Asn Ser	
300 305 310	
tcc tgg gcc cct gtg gcc cca ggg aca gtt gtg gtt agc cgt atc att	1014
Ser Trp Ala Pro Val Ala Pro Gly Thr Val Val Val Ser Arg Ile Ile	
315 320 325	

gtg tgg gac atc atg gcc ttc aat ggc atc atc cat gct ctg gcc agc Val Trp Asp Ile Met Ala Phe Asn Gly Ile Ile His Ala Leu Ala Ser	1062
330 335 340	
ccc ctc ctg gca ccc cca cag ccc cag gca gtg ctg gcg cnt gaa gcc Pro Leu Leu Ala Pro Pro Gln Pro Gln Ala Val Leu Ala Xaa Glu Ala	1110
345 350 355 360	
cca cct gtg gcg gca ggc gtg ggg gct gtg ctt gcc gct gga gca ctg Pro Pro Val Ala Ala Gly Val Gly Ala Val Leu Ala Ala Gly Ala Leu	1158
365 370 375	
ctt ggc ttg gtg gcc gga gct ctc tac ctc cgt gcc cga ggc aag ccc Leu Gly Leu Val Ala Gly Ala Leu Tyr Leu Arg Ala Arg Gly Lys Pro	1206
380 385 390	
atg ggc ttt ggc ttc tct gcc ttc cag gcg gaa gat gat gct gat gac Met Gly Phe Gly Phe Ser Ala Phe Gln Ala Glu Asp Asp Ala Asp Asp	1254
395 400 405	
gan ttc tca ccg tgg caa gaa ggg acc aac ccc acn ttg gtn tnt gtc Xaa Phe Ser Pro Trp Gln Glu Gly Thr Asn Pro Xaa Leu Xaa Xaa Val	1302
410 415 420	
ccc aac cct gtc ttt ggc agc gac acc ttt tgt gaa ccc ttc gat gac Pro Asn Pro Val Phe Gly Ser Asp Thr Phe Cys Glu Pro Phe Asp Asp	1350
425 430 435 440	
tca ctg ctg gag gag gac ttc cct gac acc cag agg atc ctc aca gtc Ser Leu Leu Glu Glu Asp Phe Pro Asp Thr Gln Arg Ile Leu Thr Val	1398
445 450 455	
aag tga cgaggctggg gctgaaagca gaagcatgca cagggaggag accantttta Lys	1454
ttgcttgtct gggtgatgg ggcaggaggg nctgagggcc tgtccagac aatannngtn	1514
ccctcgag	1522

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20 25 30

Glu His Ala Asn Cys Leu Ser Thr Gly Leu Asn Thr Arg Arg Cys Glu
35 40 45

Cys His Ala Gly Tyr Val Gly Asp Gly Leu Gln Cys Leu Glu Glu Ser
50 55 60

Glu Pro Pro Val Asp Arg Cys Leu Gly Gln Pro Pro Pro Cys His Ser
65 70 75 80

Asp Ala Met Cys Thr Asp Leu His Phe Gln Glu Lys Arg Ala Gly Val
85 90 95

Phe His Leu Gln Ala Thr Ser Gly Pro Tyr Gly Leu Asn Phe Ser Glu
100 105 110

Ala Glu Ala Ala Cys Glu Ala Gln Gly Ala Val Leu Ala Ser Phe Pro
115 120 125

Gln Leu Ser Ala Ala Gln Gln Leu Gly Phe His Leu Cys Leu Met Gly
130 135 140

Trp Leu Ala Asn Gly Ser Thr Ala His Pro Val Val Phe Pro Val Ala
145 150 155 160

Asp Cys Gly Asn Gly Arg Val Gly Ile Val Ser Leu Gly Ala Arg Lys
165 170 175

Asn Leu Ser Glu Arg Trp Asp Ala Tyr Cys Phe Arg Val Gln Asp Val
180 185 190

Ala Cys Arg Cys Arg Asn Gly Phe Val Gly Asp Gly Ile Ser Thr Cys
195 200 205

Asn Gly Lys Leu Leu Asp Val Leu Ala Ala Thr Ala Asn Phe Ser Thr
210 215 220

Phe Tyr Gly Met Leu Leu Gly Tyr Ala Asn Ala Thr Gln Arg Gly Leu
225 230 235 240

Asp Phe Leu Asp Phe Leu Asp Asp Glu Leu Thr Tyr Lys Thr Leu Phe
245 250 255

Val Pro Val Asn Glu Gly Phe Val Asp Asn Met Thr Leu Ser Gly Pro
260 265 270

Asn Leu Glu Leu His Ala Ser Asn Ala Thr Leu Leu Ser Ala Asn Ala
275 280 285

Ser Gln Gly Lys Leu Leu Pro Ala His Ser Gly Leu Ser Leu Ile Ile
290 295 300

Ser Asp Ala Gly Pro Asp Asn Ser Ser Trp Ala Pro Val Ala Pro Gly
305 310 315 320

Thr Val Val Val Ser Arg Ile Ile Val Trp Asp Ile Met Ala Phe Asn
325 330 335

Gly Ile Ile His Ala Leu Ala Ser Pro Leu Leu Ala Pro Pro Gln Pro
340 345 350

Gln Ala Val Leu Ala Xaa Glu Ala Pro Pro Val Ala Ala Gly Val Gly
355 360 365

Ala Val Leu Ala Ala Gly Ala Leu Leu Gly Leu Val Ala Gly Ala Leu
370 375 380

Tyr Leu Arg Ala Arg Gly Lys Pro Met Gly Phe Gly Phe Ser Ala Phe
385 390 395 400

Gln Ala Glu Asp Asp Ala Asp Asp Xaa Phe Ser Pro Trp Gln Glu Gly
405 410 415

Thr Asn Pro Xaa Leu Xaa Xaa Val Pro Asn Pro Val Phe Gly Ser Asp
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Asp Thr Gln Arg Ile Leu Thr Val Lys
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<211> 193

<212> PRT

<213> Homo sapiens

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Ala Ala Lys Ala Val Cys Gly Gly His Ala Thr Tyr Lys Ala Ala Arg
35 40 45

Lys Gly His Val Cys Ala Ala Gly Trp Met Ala Lys Gly Arg Val Gly
50 55 60

Tyr Val Lys Gly Asn Cys Gly Gly Lys Thr Gly Asp Tyr Gly Arg Asn
65 70 75 80

Arg Ser Arg Trp Asp Ala Tyr Cys Tyr Asn His Ala Lys Cys Gly Gly
85 90 95

Val Thr Asp Lys Arg Lys Ser Gly Asn Tyr Asp Asn Cys Tyr Trp His
100 105 110

Arg Lys Tyr Gly Arg His Ser Asp Asp Asp Gly Cys Ala Asp Tyr
115 120 125

Val Tyr Asp Ser Tyr Asp Asp Val His Gly Val Gly Arg Tyr Cys Gly
130 135 140

Asp Asp Asp Ser Thr Gly Asn Val Met Thr Lys Ser Asp Ala Ser Val
145 150 155 160

Thr Ala Gly Gly Lys Tyr Val Ala Met Asp Val Ser Lys Ser Ser Gly
165 170 175

Lys Asn Thr Ser Thr Ser Thr Gly Asn Lys Asn Ala Gly Arg Ser
180 185 190

His

<210> 7

<211> 985

<212> DNA

<213> Homo sapiens

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cctggggacg tttggccctgg ggccccagcc tggcccggtt caccctggca tgaggag 117

atg ggc ctg ttg ctc ctg gtc cca ttg ctc ctg ctg ccc ggc tcc tac 165
Met Gly Leu Leu Leu Leu Val Pro Leu Leu Leu Pro Gly Ser Tyr
1 5 10 15

gga ctg ccc ttc tac tac ggc ttc tac tac tcc aac agc gcc aac gac 213
Gly Leu Pro Phe Tyr Tyr Gly Phe Tyr Ser Asn Ser Ala Asn Asp
20 25 30

cag aac cta ggc aac ggt cat ggc aaa gac cta ctt aat gga gtg aag 261
Gln Asn Leu Gly Asn Gly His Gly Lys Asp Leu Xaa Asn Gly Val Lys
35 40 45

ctg gtg gtg gag aca ccc gag gag acc ctg ttc acc tac ctt ctt ggg gcc 309
Leu Val Val Glu Thr Pro Glu Glu Thr Leu Phe Thr Tyr Gln Gly Ala
50 55 60

agt gtg atc ctg ccc tgc cgc tac cgc tac gag ccg gcc ctg gtc tcc 357
Ser Val Ile Leu Pro Cys Arg Tyr Arg Tyr Glu Pro Ala Leu Val Ser
65 70 75 80

ccg	cg	cg	gt	gt	gt	aaa	tgg	tgg	aag	ctg	tcg	gag	aac	ggg	gcc	405	
Pro	Arg	Arg	Val	Arg	Val	Lys	Trp	Trp	Lys	Leu	Ser	Glu	Asn	Gly	Ala		
85										90				95			
cca	gag	aag	gac	gt	gt	gt	gcc	atc	ggg	ctg	agg	cac	cgc	tcc	ttt	453	
Pro	Glu	Lys	Asp	Val	Leu	Val	Ala	Ile	Gly	Leu	Arg	His	Arg	Ser	Phe		
100								105				110					
ggg	gac	ta	ca	ggc	cgc	gt	gt	ca	ctg	cg	cag	gac	aaa	gag	cat	gac	501
Gly	Asp	Tyr	Gln	Gly	Arg	Val	His	Leu	Arg	Gln	Asp	Lys	Glu	His	Asp		
115								120				125					
gtc	tcg	ntg	gag	atc	cag	gnt	ctg	cg	ctg	gag	gac	tat	ggg	cgt	ta	549	
Val	Ser	Xaa	Glu	Ile	Gln	Xaa	Leu	Arg	Leu	Glu	Asp	Tyr	Gly	Arg	Tyr		
130							135				140						
cgc	tgt	gag	gtc	atn	gac	ggg	ctg	gag	gat	gaa	agc	ggt	ctg	gt	gag	597	
Arg	Cys	Glu	Val	Xaa	Asp	Gly	Leu	Glu	Asp	Glu	Ser	Gly	Leu	Val	Glu		
145							150			155			160				
ctg	gag	ctg	cg	gg	gt	gt	gt	ttt	cct	ta	cag	tcc	ccc	aac	ggg	cgc	645
Leu	Glu	Leu	Arg	Gly	Val	Val	Phe	Pro	Tyr	Gln	Ser	Pro	Asn	Gly	Arg		
165							170			175							
ta	cag	ttc	aa	ttc	ca	ca	gg	ca	ca	g	tc	tgt	gca	ga	ca	g	693
Tyr	Gln	Phe	Asn	Phe	His	Glu	Gly	Gln	Gln	Val	Cys	Ala	Glu	Gln	Ala		
180							185			190							
gcg	gt	gt	gg	ttt	gag	ca	tc	tc	cg	gg	cc	tgg	ga	ga	gg	741	
Ala	Val	Val	Ala	Ser	Phe	Glu	Gln	Leu	Phe	Arg	Ala	Trp	Glu	Glu	Gly		
195							200			205							
ctg	ga	tgg	tg	aa	gc	gg	tgg	ctg	ca	ga	tc	ac	gt	ca	tg	789	
Leu	Asp	Trp	Cys	Asn	Ala	Gly	Trp	Leu	Gln	Asp	Ala	Thr	Val	Gln	Tyr		
210							215			220							
ccc	atc	atg	tt	ccc	cg	ca	cc	tc	gg	gg	cc	gac	ctg	gca	cct	837	
Pro	Ile	Met	Leu	Pro	Arg	Gln	Pro	Cys	Gly	Gly	Pro	Asp	Leu	Ala	Pro		
225							230			235			240				

ggc gtc cga agc tac ggc ccc cgc cac cgc ctg cac cgc tat gat 885
Gly Val Arg Ser Tyr Gly Pro Arg His Arg Arg Leu His Arg Tyr Asp
245 250 255

gta ttc tgc ttc gct act gcc ctc arg ggg cgg gtc tac tac ctg gan 933
Val Phe Cys Phe Ala Thr Ala Leu Xaa Gly Arg Val Tyr Tyr Leu Xaa
260 265 270

cac cct gag aan ctg acn ctg aca naa gca agg gaa gcc tgc caa gaa 981
His Pro Glu Xaa Leu Xaa Leu Thr Xaa Ala Arg Glu Ala Cys Gln Glu
275 280 285

aaa t 985
Lys

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20 25 30

Gln Asn Leu Gly Asn Gly His Gly Lys Asp Leu Xaa Asn Gly Val Lys
35 40 45

Leu Val Val Glu Thr Pro Glu Glu Thr Leu Phe Thr Tyr Gln Gly Ala
50 55 60

Ser Val Ile Leu Pro Cys Arg Tyr Arg Tyr Glu Pro Ala Leu Val Ser
65 70 75 80

Pro Arg Arg Val Arg Val Lys Trp Trp Lys Leu Ser Glu Asn Gly Ala
85 90 95

Pro Glu Lys Asp Val Leu Val Ala Ile Gly Leu Arg His Arg Ser Phe
100 105 110

Gly Asp Tyr Gln Gly Arg Val His Leu Arg Gln Asp Lys Glu His Asp
115 120 125

Val Ser Xaa Glu Ile Gln Xaa Leu Arg Leu Glu Asp Tyr Gly Arg Tyr
130 135 140

Arg Cys Glu Val Xaa Asp Gly Leu Glu Asp Glu Ser Gly Leu Val Glu
145 150 155 160

Leu Glu Leu Arg Gly Val Val Phe Pro Tyr Gln Ser Pro Asn Gly Arg
165 170 175

Tyr Gln Phe Asn Phe His Glu Gly Gln Gln Val Cys Ala Glu Gln Ala
180 185 190

Ala Val Val Ala Ser Phe Glu Gln Leu Phe Arg Ala Trp Glu Glu Gly
195 200 205

Leu Asp Trp Cys Asn Ala Gly Trp Leu Gln Asp Ala Thr Val Gln Tyr
210 215 220

Pro Ile Met Leu Pro Arg Gln Pro Cys Gly Gly Pro Asp Leu Ala Pro
225 230 235 240

Gly Val Arg Ser Tyr Gly Pro Arg His Arg Arg Leu His Arg Tyr Asp
245 250 255

Val Phe Cys Phe Ala Thr Ala Leu Xaa Gly Arg Val Tyr Tyr Leu Xaa
260 265 270

His Pro Glu Xaa Leu Xaa Leu Thr Xaa Ala Arg Glu Ala Cys Gln Glu
275 280 285

Lys

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<211> 355
<212> PRT
<213> Homo sapiens

<400> 9

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Pro His Pro Asp Asn Ser Ser Leu Glu His Glu Arg Ile Ile His Ile
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Gln Glu Glu Asn Gly Pro Arg Leu Leu Val Val Ala Glu Gln Ala Lys
35 40 45

Ile Phe Ser Gln Arg Gly Gly Asn Val Thr Leu Pro Cys Lys Phe Tyr
50 55 60

His Glu His Thr Ser Thr Ala Gly Ser Gly Thr His Lys Ile Arg Val
65 70 75 80

Lys Trp Thr Lys Leu Thr Ser Asp Tyr Leu Lys Glu Val Asp Val Phe
85 90 95

Val Ala Met Gly His His Arg Lys Ser Tyr Gly Lys Tyr Gln Gly Arg
100 105 110

Val Phe Leu Arg Glu Ser Ser Glu Asn Asp Ala Ser Leu Ile Ile Thr
115 120 125

Asn Ile Met Leu Glu Asp Tyr Gly Arg Tyr Lys Cys Glu Val Ile Glu
130 135 140

Gly Leu Glu Asp Asp Thr Ala Val Val Ala Leu Asn Leu Glu Gly Val
145 150 155 160

Val Phe Pro Tyr Ser Pro Arg Leu Gly Arg Tyr Asn Leu Asn Phe His
165 170 175

Glu Ala Gln Gln Ala Cys Leu Asp Gln Asp Ser Ile Ile Ala Ser Phe
180 185 190

Asp Gln Leu Tyr Glu Ala Trp Arg Ser Gly Leu Asp Trp Cys Asn Ala
195 200 205

Gly Trp Leu Ser Asp Gly Ser Val Gln Tyr Pro Ile Thr Lys Pro Arg
210 215 220

Glu Pro Cys Gly Gly Lys Asn Thr Val Pro Gly Val Arg Asn Tyr Gly
225 230 235 240

Phe Trp Asp Lys Glu Arg Ser Arg Tyr Asp Val Phe Cys Phe Thr Ser
245 250 255

Asn Phe Asn Gly Arg Phe Tyr Tyr Leu Ile His Pro Thr Lys Leu Thr
260 265 270

Tyr Asp Glu Ala Val Gln Ala Cys Leu Lys Asp Gly Ala Gln Ile Ala
275 280 285

Lys Val Gly Gln Ile Phe Ala Ala Trp Lys Leu Leu Gly Tyr Asp Arg
290 295 300

Cys Asp Ala Gly Trp Leu Ala Asp Gly Ser Val Arg Tyr Pro Ile Ser
305 310 315 320

Arg Pro Arg Lys Arg Cys Ser Pro Asn Glu Ala Ala Val Arg Phe Val
325 330 335

Gly Phe Pro Asp Lys Lys His Lys Leu Tyr Gly Val Tyr Cys Phe Arg
340 345 350

Ala Tyr Asn
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gccagatgct cccagaaggg cacgaaggc tcctgcagct gccagaaggg atacaaaggg 120
gacgggcaca gctgcacaga gatagacccc tgtgcagacg gccttaacgg agggtgtcac 180
gagcacgcca cctgttaag atg aca ggc ccg ggc aag cac aag tgt gag tgt 231
Met Thr Gly Pro Gly Lys His Lys Cys Glu Cys
1 5 10

aaa agt cac tat gtc gga gat ggg ctg aac tgt gag ccg gag cag ctg 279
Lys Ser His Tyr Val Gly Asp Gly Leu Asn Cys Glu Pro Glu Gln Leu
15 20 25

ccc att gac cgc tgc tta cag gac aat ggg cag tgc cat gca gac gcc 327
Pro Ile Asp Arg Cys Leu Gln Asp Asn Gly Gln Cys His Ala Asp Ala
30 35 40

aaa tgt gtc gac ctc cac ttc cag gat acc act gtt ggg gtg ttc cat 375
Lys Cys Val Asp Leu His Phe Gln Asp Thr Thr Val Gly Val Phe His
45 50 55

cta cgc tcc cca ctg ggc cag tat aag ctg acc ttt gac aaa gcc aga	423
Leu Arg Ser Pro Leu Gly Gln Tyr Lys Leu Thr Phe Asp Lys Ala Arg	
60 65 70 75	
gag gcc tgt gcc aac gaa gct gcg acc atg gca acc tac aac cag ctc	471
Glu Ala Cys Ala Asn Glu Ala Ala Thr Met Ala Thr Tyr Asn Gln Leu	
80 85 90	
tcc tat nnc cag aag gcc aag tac cac ctg tgc tca gca ggc tgg ctg	519
Ser Tyr Xaa Gln Lys Ala Lys Tyr His Leu Cys Ser Ala Gly Trp Leu	
95 100 105	
gag acc ggg cgg gtt gcc tac ccc aca gcc ttc gcc tcc cag aac tgt	567
Glu Thr Gly Arg Val Ala Tyr Pro Thr Ala Phe Ala Ser Gln Asn Cys	
110 115 120	
ggc tct ggt gtg gtt ggg ata gtg gac tat gga cct aga ccc aac aag	615
Gly Ser Gly Val Val Gly Ile Val Asp Tyr Gly Pro Arg Pro Asn Lys	
125 130 135	
agt gaa atg tgg gat gtc ttc tgc tat cgg atg aaa gat gtg aac tgc	663
Ser Glu Met Trp Asp Val Phe Cys Tyr Arg Met Lys Asp Val Asn Cys	
140 145 150 155	
acc tnc aag gtg ggc tat gtg gga gat ggc ttc tca tac agt ggg aac	711
Thr Xaa Lys Val Gly Tyr Val Gly Asp Gly Phe Ser Tyr Ser Gly Asn	
160 165 170	
ctg ctg cag gtc ctg atg tcc ttc ccc tca ctc aca aac ttc ctg acg	759
Leu Leu Gln Val Leu Met Ser Phe Pro Ser Leu Thr Asn Phe Leu Thr	
175 180 185	
gaa gtg ctg gcc tat tcc aac agc tca gct cga ggc cgt gca ttt cta	807
Glu Val Leu Ala Tyr Ser Asn Ser Ser Ala Arg Gly Arg Ala Phe Leu	
190 195 200	
gaa cac ctg act gac ctg tcc atc cgc ggc acc ctc ttt gtn cca cag	855
Glu His Leu Thr Asp Leu Ser Ile Arg Gly Thr Leu Phe Val Pro Gln	
205 210 215	

aac agt ggg ctg ggg gag aat gag acc ttg tct ggg cgg gac atc gag	903
Asn Ser Gly Leu Gly Glu Asn Glu Thr Leu Ser Gly Arg Asp Ile Glu	
220 225 230 235	
cac cac ctc gcc aat gtc agc atg ttt ttc tac aat gac ctt gtc aat	951
His His Leu Ala Asn Val Ser Met Phe Phe Tyr Asn Asp Leu Val Asn	
240 245 250	
ggc acc acc ctg caa acg agg ctg gga agc aag ctg ctc atc act gac	999
Gly Thr Thr Leu Gln Thr Arg Leu Gly Ser Lys Leu Leu Ile Thr Asp	
255 260 265	
aga cag gag cca ctc cac ccg acg gag acc agg tgt gtt gat gga aga	1047
Arg Gln Asp Pro Leu His Pro Thr Glu Thr Arg Cys Val Asp Gly Arg	
270 275 280	
gac act ctg gag tgg gac atc tgt gcc tcc aat ggg atc aca cat gtc	1095
Asp Thr Leu Glu Trp Asp Ile Cys Ala Ser Asn Gly Ile Thr His Val	
285 290 295	
att tcc agg yct tta aaa gca ccc cct gcc ccc gtg acc ttg ncc cac	1143
Ile Ser Arg Xaa Leu Lys Ala Pro Pro Ala Pro Val Thr Leu Xaa His	
300 305 310 315	
act ggn ttg gga gna ggg atc ttc tnt gnc atc atc ctg gtg act ggg	1191
Thr Gly Leu Gly Xaa Gly Ile Phe Xaa Xaa Ile Ile Leu Val Thr Gly	
320 325 330	
gct gtt gcc ttg gct gct tac tcc tac ttt cgg ata aac cgg aaa aca	1239
Ala Val Ala Leu Ala Ala Tyr Ser Tyr Phe Arg Ile Asn Arg Lys Thr	
335 340 345	
atc ggc ttc can cat ttt ga	1259
Ile Gly Phe Xaa His Phe	
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Gly Asp Gly Leu Asn Cys Glu Pro Glu Gln Leu Pro Ile Asp Arg Cys
20 25 30

Leu Gln Asp Asn Gly Gln Cys His Ala Asp Ala Lys Cys Val Asp Leu
35 40 45

His Phe Gln Asp Thr Thr Val Gly Val Phe His Leu Arg Ser Pro Leu
50 55 60

Gly Gln Tyr Lys Leu Thr Phe Asp Lys Ala Arg Glu Ala Cys Ala Asn
65 70 75 80

Glu Ala Ala Thr Met Ala Thr Tyr Asn Gln Leu Ser Tyr Xaa Gln Lys
85 90 95

Ala Lys Tyr His Leu Cys Ser Ala Gly Trp Leu Glu Thr Gly Arg Val
100 105 110

Ala Tyr Pro Thr Ala Phe Ala Ser Gln Asn Cys Gly Ser Gly Val Val
115 120 125

Gly Ile Val Asp Tyr Gly Pro Arg Pro Asn Lys Ser Glu Met Trp Asp
130 135 140

Val Phe Cys Tyr Arg Met Lys Asp Val Asn Cys Thr Xaa Lys Val Gly
145 150 155 160

Tyr Val Gly Asp Gly Phe Ser Tyr Ser Gly Asn Leu Leu Gln Val Leu
165 170 175

Met Ser Phe Pro Ser Leu Thr Asn Phe Leu Thr Glu Val Leu Ala Tyr
180 185 190

Ser Asn Ser Ser Ala Arg Gly Arg Ala Phe Leu Glu His Leu Thr Asp
195 200 205

Leu Ser Ile Arg Gly Thr Leu Phe Val Pro Gln Asn Ser Gly Leu Gly
210 215 220

Glu Asn Glu Thr Leu Ser Gly Arg Asp Ile Glu His His Leu Ala Asn
225 230 235 240

Val Ser Met Phe Phe Tyr Asn Asp Leu Val Asn Gly Thr Thr Leu Gln
245 250 255

Thr Arg Leu Gly Ser Lys Leu Leu Ile Thr Asp Arg Gln Asp Pro Leu
260 265 270

His Pro Thr Glu Thr Arg Cys Val Asp Gly Arg Asp Thr Leu Glu Trp
275 280 285

Asp Ile Cys Ala Ser Asn Gly Ile Thr His Val Ile Ser Arg Xaa Leu
290 295 300

Lys Ala Pro Pro Ala Pro Val Thr Leu Xaa His Thr Gly Leu Gly Xaa
305 310 315 320

Gly Ile Phe Xaa Xaa Ile Ile Leu Val Thr Gly Ala Val Ala Leu Ala
325 330 335

Ala Tyr Ser Tyr Phe Arg Ile Asn Arg Lys Thr Ile Gly Phe Xaa His
340 345 350

Phe

<210> 12

<211> 275

<212> PRT

<213> Mus musculus

<400> 12

Met Val Val Leu Leu Cys Leu Cys Val Leu Leu Trp Glu Glu Ala His
1 5 10 15

Gly Trp Gly Phe Lys Asn Gly Ile Phe His Asn Ser Ile Trp Leu Glu
20 25 30

Gln Ala Ala Gly Val Tyr His Arg Glu Ala Arg Ala Gly Arg Tyr Lys
35 40 45

Leu Thr Tyr Ala Glu Ala Lys Ala Val Cys Glu Phe Glu Gly Gly Arg
50 55 60

Leu Ala Thr Tyr Lys Gln Leu Glu Ala Ala Arg Lys Ile Gly Phe His
65 70 75 80

Val Cys Ala Ala Gly Trp Met Ala Lys Gly Arg Val Gly Tyr Pro Ile
85 90 95

Val Lys Pro Gly Pro Asn Cys Gly Phe Gly Lys Thr Gly Ile Ile Asp
100 105 110

Tyr Gly Ile Arg Leu Asn Arg Ser Glu Arg Trp Asp Ala Tyr Cys Tyr
115 120 125

Asn Pro His Ala Lys Glu Cys Gly Gly Val Phe Thr Asp Pro Lys Arg
130 135 140

Ile Phe Lys Ser Pro Gly Phe Pro Asn Glu Tyr Asp Asp Asn Gln Val
145 150 155 160

Cys Tyr Trp His Ile Arg Leu Lys Tyr Gly Gln Arg Ile His Leu Ser
165 170 175

Phe Leu Asp Phe Asp Leu Glu His Asp Pro Gly Cys Leu Ala Asp Tyr
180 185 190

Val Glu Ile Tyr Asp Ser Tyr Asp Asp Val His Gly Phe Val Gly Arg
195 200 205

Tyr Cys Gly Asp Glu Leu Pro Glu Asp Ile Ile Ser Thr Gly Asn Val
210 215 220

Met Thr Leu Lys Phe Leu Ser Asp Ala Ser Val Thr Ala Gly Gly Phe
225 230 235 240

Gln Ile Lys Tyr Val Thr Val Asp Pro Ala Ser Lys Ser Ser Gln Ala
245 250 255

Lys Asn Thr Ser Thr Thr Gly Asn Lys Lys Phe Leu Pro Gly Arg Phe
260 265 270

Ser His Leu
275

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<220>
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44

<210> 14
<211> 44
<212> DNA
<213> artificial sequence

<220>
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gcagcatcta gatcaattga ctgtgaggat cctctgggtg tcag

44

<210> 15
<211> 45
<212> DNA
<213> artificial sequence

<220>
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45

<210> 16
<211> 45
<212> DNA
<213> artificial sequence

<220>
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<210> 17
<211> 48
<212> DNA
<213> artificial sequence

<220>
<223> contains an EcoRI restriction site

<400> 17
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<210> 18
<211> 46
<212> DNA
<213> artificial sequence

<220>
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<222> (40)
<223> n equals a, t, g or c

<220>
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<210> 19
<211> 44
<212> DNA
<213> artificial sequence

<220>
<223> contains an EcoRI restriction site

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<210> 20	
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<210> 21	
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<400> 21	
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<210> 22	
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<210> 23
<211> 51
<212> DNA
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<220>
<223> contains a BglII restriction site

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<210> 24
<211> 45
<212> DNA
<213> artificial sequence

<220>
<223> contains an XbaI restriction site

<400> 24
gcagcatcta gatcacttga ctgtgaggat cctctgggtg tcagg 45

<210> 25
<211> 54
<212> DNA
<213> artificial sequence

<220>
<223> contains a BglII restriction site

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<210> 26
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<220>
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<210> 27
<211> 50
<212> DNA
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<220>
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<400> 27
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<210> 28
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<220>
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<220>
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<210> 29
<211> 50
<212> DNA
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<220>
<223> contains a BamHI restriction site

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<210> 30
<211> 44
<212> DNA
<213> artificial sequence

<220>
<223> contains an XbaI restriction site

<400> 30
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<210> 31
<211> 54
<212> DNA
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<220>
<223> contains a BamHI restriction site

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<210> 32
<211> 45
<212> DNA
<213> artificial sequence

<220>
<223> contains an XbaI restriction site

<400> 32
gcagcatcta gatcaattga ctgtgaggat cctctgggtg tcagg 45

<210> 33
<211> 54
<212> DNA
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<220>
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<210> 34
<211> 46
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<220>
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<210> 35
<211> 50
<212> DNA
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<220>
<223> contains a BamHI restriction site

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<211> 49
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<220>
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<223> n equals a, t, g or c

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<400> 36

gcagcatcta gatcaaaaatg ntggaagccg attgtttcc ggttatcc 49

<210> 37

<211> 733

<212> DNA

<213> Homo sapiens

<400> 37

gggatccgga gcccaaatct tctgacaaaa ctcacacatg cccaccgtgc ccagcacctg 60

aattcgaggg tgaccgtca gtcttctct tccccccaaa acccaaggac accctcatga 120

tctcccgac tcctgaggtc acatgcgtgg tggtgacgt aagccacgaa gaccctgagg 180

tcaagttcaa ctggtacgta gacggcgtgg aggtgcataa tgccaagaca aagccgcggg 240

aggagcagta caacagcagc taccgtgtgg tcagcgtcct caccgtcctg caccaggact 300

ggctgaatgg caaggagtac aagtgcagg tctccaacaa agccctccca acccccacatcg 360

agaaaaccat ctccaaagcc aaagggcagc cccgagaacc acaggtgtac accctgcccc 420

catcccgaa ttagctgacc aagaaccagg tcagcctgac ctgcctggc aaaggcttct 480

atccaagcga catcgccgtg gagtgggaga gcaatggca gccggagaac aactacaaga 540

ccacgcctcc cgtgctggac tccgacggct ctttttctt ctacagcaag ctcaccgtgg 600

acaagagcag gtggcagcag gggaaacgtct tctcatgctc cgtgatgcat gaggctctgc 660

acaaccacta cacgcagaag agcctctccc tgtctccggg taaatgagtg cgacggccgc 720

gactctagag gat 733.